## **CLAIMS**

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1.	A method for detecting the presence of at least one selected strain of an
orga	anism in a sample, comprising the steps of:

providing a sample that may comprise nucleic acid from at least one selected strain of an organism and nucleic acid from at least one non-selected strain of the organism;

providing a plurality of primers substantially complementary to regions of both said nucleic acid from at least one selected strain of the organism and said nucleic acid from at least one non-selected strain of the organism;

exposing said sample to at least one probe that is sufficiently complementary to a portion of said nucleic acid from at least one non-selected strain to block full length amplification of said nucleic acid from at least one non-selected strain between said plurality of primers, said at least one probe comprising a nucleic acid analog;

amplifying said nucleic acid from at least one selected strain between said plurality of primers; and

detecting amplification product of nucleic acid from at least one selected strain.

- 2. The method of claim 1, wherein said at least one selected strain comprises a pathogenic strain.
- 1 3. The method of claim 2, wherein said sample is derived from a subject and said pathogenic strain indicates a risk of cancerous growth in said subject.
- 1 4. The method of claim 1, wherein said organism comprises human papilloma virus (HPV).
  - 5. The method of claim 1, wherein said at least one probe comprises PNA.

- 1 6. The method of claim 5, wherein said at least one probe further comprises a nucleotide different from PNA.
- 7. The method of claim 1, wherein each of said at least one probe comprises at least 8 bases.
- 1 8. The method of claim 1, wherein the step of amplifying said nucleic acid of at
- least one selected strain between said plurality of primers comprises conducting a
- reaction selected from the group consisting of a polymerase chain reaction, a ligase
- chain reaction, a rolling circle replication, a branched chain amplification, a nucleic
- 5 acid based sequence amplification (NASBA), a Cleavase Fragment Length
- 6 Polymorphism, ICAN and RAM.
- 9. The method of claim 4, wherein said regions of both said nucleic acids are parts of a region selected from the group consisting of L1, L2, E1, E6, and E7 region.
- 1 10. The method of claim 4, wherein said at least one non-selected strain equals
- 2 all the low-risk HPV strains known.
- 1 11. The method of claim 4, wherein said at least one non-selected strain is
- selected from the group consisting of HPV strains 6, 11, 42, 43, and 44.
- 1 12. The method of claim 4, wherein said at least one selected strain comprises a
- 2 plurality of high-risk HPV strains.
- 1 13. The method of claim 4, wherein said plurality of primers comprise MY09 and
- 2 MY11 (SEQ. ID. NOS. 10 and 11).
- 1 14. The method of claim 4, wherein said at least one probe is selected from the
- group of sequences consisting of SEQ. ID. NO. 6 and SEQ. ID. NO. 7.
- 1 15. The method of claim 1, wherein said sample is a cervical scraping.

1	16.	The method of claim 1, wherein said step of detecting amplification product					
2	compr	comprises in-gel electrophoresis of said product and staining said product with					
3	ethidiu	um bromide.					
1	17.	A method for detecting the presence of a target nucleic acid of a human					
2	papillo	papilloma virus (HPV) in a sample cell, comprising the steps of:					
3		suspending a sample cell in a solution;					
4		isolating a target nucleic acid of a HPV from said sample cell;					
5	contac	ting said target nucleic acid with at least one probe comprising peptide nucleic					
6	acid (I	acid (PNA), said at least one probe being substantially complementary to portions of					
7	nuclei	nucleic acids of multiple HPV types; and					
8	dete	detecting hybridization between said at least one probe and said target nucleic					
9	acid.						
1	18.	The method of claim 1, wherein said solution contains an alcohol in an					
2	amour	amount sufficient to fix sample cells without coagulation, an anti-clumping agent,					
3	and a	and a buffer agent that maintains the solution at a pH within a range of about 4 to					
4	about	7.					
1	19.	The method of claim 1, wherein said sample cells come from a subject and					
2	where	in the presence of said target nucleic acid sequence indicates a risk of tumor					
3	growt	growth in said subject.					
1	20.	The method of claim 4, wherein said tumorous growth is associated with					

- 1 20. The method of claim 4, wherein said tumorous growth is associated with either cervical cancer or endocervical carcinoma.
- 1 21. The method of claim 3, wherein the presence of said target nucleic acid sequence is indicative of the presence of a particular type of HPV.
- The method of claim 7, wherein said particular type of HPV is selected from the group consisting of types 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 68 and 70.

- 1 23. The method of claim 3, wherein absence of said target nucleic acid sequence
- 2 is diagnostic of absence of infection by HPV.
- 1 24. The method of claim 3, wherein absence of said target nucleic acid sequence
- 2 is diagnostic of absence of infection by HPV types selected from the group
- 3 consisting of types 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 68 and 70.
- 1 25. The method of claim 1, wherein absence of said target nucleic acid sequence
- 2 is diagnostic of absence of infection by high-risk types of HPV.
- 1 26. The method of claim 1, further comprising amplification of said target
- 2 nucleic acid.
- 1 27. The method of claim 12, wherein said amplification step comprises
- 2 conducting a polymerase chain reaction.
- 1 28. The method of claim 1, further comprising capturing said target nucleic acid
- 2 onto a solid support through PNA-DNA interaction.
- The method of claim 1, wherein each of said at least one probe comprises at
- 2 least 8 bases.
- The method of claim 1, wherein said at least one probe comprises a
- 2 nucleotide different from PNA.
- The method of claim 1, wherein said at least one probe is selected from the
- 2 group consisting of SEQ. ID. NOS. 1-5.
- The method of claim 1, wherein said at least one probe is labeled with a
- 2 detectable marker.
- The method of claim 17 wherein said at least one probe comprises a
- 2 molecular beacon probe.

1	34.	The method of claim 1, further comprising using an antibody to recognize
2	said hy	bridization.
1	35.	A method for detecting the presence of a target nucleic acid of a human
2	papillo	ma virus (HPV) in a sample, comprising the steps of:
3		capturing candidate nucleic acids that include a target nucleic acid on a solic
4	suppor	t;
5		contacting said candidate nucleic acids with at least one probe comprising
6	peptide	e nucleic acid (PNA), said at least one probe being substantially
7	comple	ementary to portions of nucleic acids of multiple HPV types; and
8		detecting hybridization between said at least one probe and a target nucleic
9	acid.	
1	36.	The method of claim 20, wherein capturing candidate nucleic acids
2	compr	ises DNA-DNA interaction.
1	37.	A method for in situ detection of the presence of a target nucleic acid of a
2	human	papilloma virus (HPV) in a sample, comprising the steps of:
3	tran	sferring suspended sample cells uniformly onto a surface;
4	in s	itu hybridizing a target nucleic acid of a HPV contained in said cells with at
5	least o	ne probe comprising peptide nucleic acid (PNA), said at least one probe being
6	substa	ntially complementary to portions of nucleic acids of multiple HPV types; and
7		detecting hybridization between said at least one probe and a target nucleic
8	acid.	